



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/826,791A

DATE: 01/29/2004

TIME: 09:38:01

Input Set : A:\PC10914A Seq Listing 1-20-04.ST25.txt
 Output Set: N:\CRF4\01292004\I826791A.raw

3 <110> APPLICANT: Pfizer Inc.
 4 Harland, Lee
 6 <120> TITLE OF INVENTION: Novel Polypeptide
 8 <130> FILE REFERENCE: PCS10914ADAM
 10 <140> CURRENT APPLICATION NUMBER: 09/826,791A
 11 <141> CURRENT FILING DATE: 2001-04-05
 13 <150> PRIOR APPLICATION NUMBER: 0008504.3
 14 <151> PRIOR FILING DATE: 2000-04-05
 16 <150> PRIOR APPLICATION NUMBER: 60/198,367
 17 <151> PRIOR FILING DATE: 2000-04-19
 19 <160> NUMBER OF SEQ ID NOS: 7
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 993
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1

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31 aagagagaat	ttttccaaat	tgtatatctg	ataatatttt	tctggggagt	cttggaaat	120									
33 gggttgtcca	tatatgttt	cctgcagcct	tataagaagt	ccacatctgt	gaacgtttc	180									
35 atgtaaattc	tggccatttc	agatctcctg	ttcataagca	cgttccctt	caggctgac	240									
37 tattatctta	gaggctcaa	ttggatattt	ggagacctgg	cctgcaggat	tatgtcttat	300									
39 tccttgatg	tcaacatgta	cagcgttatt	tatttcctga	ccgtgctgag	tgttggtcg	360									
41 ttccctggcaa	tggttcaccc	cttcggctt	ctgcatgtca	ccagcatca	gagtgcctgg	420									
43 atccctctgtg	ggatcatatg	gatccttatac	atggcttcct	caataatgct	cctggacagt	480									
45 ggctctgagc	agaacggcag	tgtcacatca	tgcttagagc	tgaatctcta	taaaattgct	540									
47 aagctgcaga	ccatgaacta	tattgccttg	gtgggtggct	gcctgctgcc	attttcaca	600									
49 ctcagcatct	gttatctgct	gatcattcgg	gttctgttaa	aagtggaggt	cccagaatcg	660									
51 gggctgcggg	tttctcacag	gaaggcactg	accaccatca	tcatcacctt	gatcatcttc	720									
53 ttcttggtt	tcctgcccta	tcacacactg	aggaccgtcc	acttgacgac	atggaaagtg	780									
55 ggtttatgca	aagacagact	gcataaaagct	ttggttatca	cactggcctt	ggcagcagcc	840									
57 aatgcctgct	tcaatccct	gctctattac	tttgctgggg	agaattttaa	ggacagacta	900									
59 aagtctgcac	tcagaaaagg	ccatccacag	aaggcaaaga	caaagtgtgt	tttccctgtt	960									
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65 <211>	LENGTH:	330													
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72 1				5				10				15			
75 Ile	Glu	Asn	Phe	Lys	Arg	Glu	Phe	Phe	Pro	Ile	Val	Tyr	Leu	Ile	Ile
76				20				25				30			

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79 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
 80 35 40 45
 83 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
 84 50 55 60
 87 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
 88 65 70 75 80
 91 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
 92 85 90 95
 95 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
 96 100 105 110
 99 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
 100 115 120 125
 103 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
 104 130 135 140
 107 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
 108 145 150 155 160
 111 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
 112 165 170 175
 115 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
 116 180 185 190
 119 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
 120 195 200 205
 123 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
 124 210 215 220
 127 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
 128 225 230 235 240
 131 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
 132 245 250 255
 135 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
 136 260 265 270
 139 Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
 140 275 280 285
 143 Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
 144 290 295 300
 147 Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
 148 305 310 315 320
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 152 325 330
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 156 <211> LENGTH: 24
 157 <212> TYPE: DNA
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 164 <210> SEQ ID NO: 4 24
 165 <211> LENGTH: 22
 166 <212> TYPE: DNA
 167 <213> ORGANISM: Homo sapiens
 169 <400> SEQUENCE: 4

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185	Met	Glu	Arg	Lys	Phe	Met	Ser	Leu	Gln	Pro	Ser	Ile	Ser	Val	Ser	Glu	
186	1					5				10					15		
188	atg	gaa	cca	aat	ggc	acc	ttc	agc	aat	aac	aac	agc	agg	aac	tgc	aca	96
189	Met	Glu	Pro	Asn	Gly	Thr	Phe	Ser	Asn	Asn	Asn	Ser	Arg	Asn	Cys	Thr	
190						20			25				30				
192	att	gaa	aac	ttc	aag	aga	gaa	ttt	ttc	cca	att	gta	tat	ctg	ata	ata	144
193	Ile	Glu	Asn	Phe	Lys	Arg	Glu	Phe	Phe	Pro	Ile	Val	Tyr	Leu	Ile	Ile	
194						35			40				45				
196	ttt	ttc	tgg	gga	gtc	ttg	gga	aat	ggg	ttt	tcc	ata	tat	gtt	ttc	ctg	192
197	Phe	Phe	Trp	Gly	Val	Leu	Gly	Asn	Gly	Leu	Ser	Ile	Tyr	Val	Phe	Leu	
198						50			55				60				
200	cag	cct	tat	aag	aag	tcc	aca	tct	gtg	aac	gtt	ttc	atg	cta	aat	ctg	240
201	Gln	Pro	Tyr	Lys	Lys	Ser	Thr	Ser	Val	Asn	Val	Phe	Met	Leu	Asn	Leu	
202	65					70			75				80				
204	gcc	att	tca	gat	ctc	ctg	ttc	ata	agc	acg	ctt	ccc	ttc	agg	gct	gac	288
205	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Ile	Ser	Thr	Leu	Pro	Phe	Arg	Ala	Asp	
206						85			90				95				
208	tat	tat	ctt	aga	ggc	tcc	aat	tgg	ata	ttt	gga	gac	ctg	gcc	tgc	agg	336
209	Tyr	Tyr	Leu	Arg	Gly	Ser	Asn	Trp	Ile	Phe	Gly	Asp	Leu	Ala	Cys	Arg	
210						100			105				110				
212	att	atg	tct	tat	tcc	ttg	tat	gtc	aac	atg	tac	agc	agt	att	tat	ttc	384
213	Ile	Met	Ser	Tyr	Ser	Leu	Tyr	Val	Asn	Met	Tyr	Ser	Ser	Ile	Tyr	Phe	
214						115			120				125				
216	ctg	acc	gtg	ctg	agt	gtt	gtg	cgt	ttc	ctg	gca	atg	gtt	cac	ccc	ttt	432
217	Leu	Thr	Val	Leu	Ser	Val	Val	Arg	Phe	Leu	Ala	Met	Val	His	Pro	Phe	
218						130			135				140				
220	cgg	ctt	ctg	cat	gtc	acc	agc	atc	agg	agt	gcc	tgg	atc	ctc	tgt	ggg	480
221	Arg	Leu	Leu	His	Val	Thr	Ser	Ile	Arg	Ser	Ala	Trp	Ile	Leu	Cys	Gly	
222	145					150			155				160				
224	atc	ata	tgg	atc	ctt	atc	atg	gct	tcc	tca	ata	atg	ctc	ctg	gac	agt	528
225	Ile	Ile	Trp	Ile	Leu	Ile	Met	Ala	Ser	Ser	Ile	Met	Leu	Leu	Asp	Ser	
226						165			170				175				
228	ggc	tct	gag	cag	aac	ggc	agt	gtc	aca	tca	tgc	tta	gag	ctg	aat	ctc	576
229	Gly	Ser	Glu	Gln	Asn	Gly	Ser	Val	Thr	Ser	Cys	Leu	Glu	Leu	Asn	Leu	
230						180			185				190				
232	tat	aaa	att	gct	aag	ctg	cag	acc	atg	aac	tat	att	gcc	ttg	gtg	gtg	624
233	Tyr	Lys	Ile	Ala	Lys	Leu	Gln	Thr	Met	Asn	Tyr	Ile	Ala	Leu	Val	Val	
234						195			200				205				
236	ggc	tgc	ctg	ctg	cca	ttt	ttc	aca	ctc	agc	atc	tgt	tat	ctg	ctg	atc	672

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237	Gly	Cys	Leu	Leu	Pro	Phe	Phe	Thr	Leu	Ser	Ile	Cys	Tyr	Leu	Leu	Ile	
238	210				215				220								
240	att	cgg	gtt	ctg	tta	aaa	gtg	gag	gtc	cca	gaa	tcg	ggg	ctg	cgg	gtt	720
241	Ile	Arg	Val	Leu	Leu	Lys	Val	Glu	Val	Pro	Glu	Ser	Gly	Leu	Arg	Val	
242	225				230				235							240	
244	tct	cac	agg	aag	gca	ctg	acc	acc	atc	atc	atc	acc	ttg	atc	atc	ttc	768
245	Ser	His	Arg	Lys	Ala	Leu	Thr	Thr	Ile	Ile	Ile	Thr	Leu	Ile	Ile	Phe	
246		245				250				255							
248	ttc	ttc	tgt	ttc	ctg	ccc	tat	cac	aca	ctg	agg	acc	gtc	cac	ttg	acg	816
249	Phe	Leu	Cys	Phe	Leu	Pro	Tyr	His	Thr	Leu	Arg	Thr	Val	His	Leu	Thr	
250		260			265				270								
252	aca	tgg	aaa	gtg	gtt	tta	tgc	aaa	gac	aga	ctg	cat	aaa	gct	ttg	gtt	864
253	Thr	Trp	Lys	Val	Gly	Leu	Cys	Lys	Asp	Arg	Leu	His	Lys	Ala	Leu	Val	
254		275			280				285								
256	atc	aca	ctg	gcc	ttg	gca	gca	aat	gcc	tgc	ttc	aat	cct	ctg	ctc		912
257	Ile	Thr	Leu	Ala	Leu	Ala	Ala	Asn	Ala	Cys	Phe	Asn	Pro	Leu	Leu		
258		290			295				300								
260	tat	tac	ttt	gct	ggg	gag	aat	ttt	aag	gac	aga	cta	aag	tct	gca	ctc	960
261	Tyr	Tyr	Phe	Ala	Gly	Glu	Asn	Phe	Lys	Asp	Arg	Leu	Lys	Ser	Ala	Leu	
262		305			310				315							320	
264	aga	aaa	ggc	cat	cca	cag	aag	gca	aag	aca	aag	tgt	gtt	ttc	cct	gtt	1008
265	Arg	Lys	Gly	His	Pro	Gln	Lys	Ala	Lys	Thr	Lys	Cys	Val	Phe	Pro	Val	
266					325				330							335	
268	agt	gtg	tgg	ttg	aga	aag	gaa	aca	aga	gtt	taa						1041
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285					20				25							30	
288	Ile	Glu	Asn	Phe	Lys	Arg	Glu	Phe	Phe	Pro	Ile	Val	Tyr	Leu	Ile	Ile	
289		35				40						45					
292	Phe	Phe	Trp	Gly	Val	Leu	Gly	Asn	Gly	Leu	Ser	Ile	Tyr	Val	Phe	Leu	
293		50				55						60					
296	Gln	Pro	Tyr	Lys	Lys	Ser	Thr	Ser	Val	Asn	Val	Phe	Met	Leu	Asn	Leu	
297	65				70				75							80	
300	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Ile	Ser	Thr	Leu	Pro	Phe	Arg	Ala	Asp	
301					85				90							95	
304	Tyr	Tyr	Leu	Arg	Gly	Ser	Asn	Trp	Ile	Phe	Gly	Asp	Leu	Ala	Cys	Arg	
305		100						105								110	
308	Ile	Met	Ser	Tyr	Ser	Leu	Tyr	Val	Asn	Met	Tyr	Ser	Ser	Ile	Tyr	Phe	
309		115				120						125					
312	Leu	Thr	Val	Leu	Ser	Val	Val	Arg	Phe	Leu	Ala	Met	Val	His	Pro	Phe	
313		130				135						140					

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316 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
 317 145 150 155 160
 320 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
 321 165 170 175
 324 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
 325 180 185 190
 328 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
 329 195 200 205
 332 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
 333 210 215 220
 336 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
 337 225 230 235 240
 340 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
 341 245 250 255
 344 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
 345 260 265 270
 348 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
 349 275 280 285
 352 Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
 353 290 295 300
 356 Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
 357 305 310 315 320
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 365 340 345
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 371 <211> LENGTH: 674
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 375 <400> SEQUENCE: 7
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 386 35 40 45
 389 Ile Lys Thr Tyr His Lys Lys Ser Ala Phe Gln Val Tyr Met Ile Asn
 390 50 55 60
 393 Leu Ala Val Ala Asp Leu Leu Cys Val Cys Thr Leu Pro Leu Arg Val
 394 65 70 75 80
 397 Val Tyr Tyr Val His Lys Gly Ile Trp Leu Phe Gly Asp Phe Leu Cys
 398 85 90 95
 401 Arg Leu Ser Thr Tyr Ala Leu Tyr Val Asn Leu Tyr Cys Ser Ile Phe
 402 100 105 110
 405 Phe Met Thr Ala Met Ser Phe Phe Arg Cys Ile Ala Ile Val Phe Pro
 406 115 120 125
 409 Val Gln Asn Ile Asn Leu Val Thr Gln Lys Lys Ala Arg Phe Val Cys
 410 130 135 140

VERIFICATION SUMMARY

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